

Table 1. Identification of peptides in AfC fractions.

Protein extract	Cssl (AnrP440134)	Hydrophobin (AnrP57221)	GAPDH (AnrP539502)	Enolase (AnrP7789)	Catalases and IMDH B
Diffusate	KVAQEIIINPGPK	FPVPDDITVK ATYAAGDVTDIDEGILAGTLK	AGISLNPNFVK TAAQNIIIPSSGAAK NILGYTEDDVSSDLNGDER	NVNETIGPALIK VNQIGTILTESIQAAK TSDFOIVGDDLLVTNPGR	Not detected
Cell surface exposed	VAQEIIINPGPK	FPVPDDITVK ATYAAGDVTDIDEGILAGTLK	Not detected	WLTYEQIADLYK Not detected	FGFDLLDPTK (Catalase B peptide AnrP977704) IX ₁ AEX ₂ ALR (IMDH B peptide)
Cell wall	KVAQEIIINPGPK VAQEIIINPGPK SISFQILDCR EGAEQSAFPQAEHSTK VVTTPYTCDOVK	FPVPDDITVK 3-12 ATYAAGDVTDIDEGILAGTLK 30-50	AGISLNPNFVK TAAQNIIIPSSGAAK NILGYTEDDVSSDLNGDER VPTSNSVVDLTCR YDTTHGQFK	Not detected	TGPSLLEDQIAR (Catalase A peptide AnrP145557)
Peptides used for Ab production	KVAQEIIINPGPKVVT KEGAEQSAPQAEHSTK	PVPDDITVKQATEKCGD ATYAAGDVTDIDEGIL	GTIETDQGLIVNGK TEDDVSSDLNGDERS FKGTIETDQGLIVNGKK	KVNNETIGPALIKENID TSDFOIVGDDLLVTNPGR	DEEDQILRFGFDLLDPTKIIVP RIDNDLARVARAIGV

Table 2. Biochemical characteristics of Csl.

	Complete	N-terminus	C-terminus
MW	28179.92	13960.38	14236.54
Residues	260	130	130
Strongly Basic (+) Amino Acids (K, R)	25	10	15
Strongly Acidic (-) Amino Acids (D, E)	33	9	24
Hydrophobic Amino Acids (A, I, L, F, W, V)	89	55	34
Polar Amino Acids (N, C, Q, S, T, Y)	70	36	34
Isoelectric Point	5.081	7.626	4.760
Charge at pH 7.0	-7.634	0.892	-8.617

Table 3. Sequence of peptides chosen for the production of multiple antigenic peptides and antisera against selected target proteins

<u>Peptide name</u>	<u>Peptide sequence</u>	<u>Parental protein</u>	<u>Reactivity vs AfC*</u>	<u>Reactivity vs AfM*</u>
GAP-B-1	FKGTLETYDQGLVNGKK (SEQ ID NO:12)	GAPDH B	++	+++
GAP-B-2	TEDDVVSDDLNGDERS (SEQ ID NO:11)	GAPDH B	+++	++
HYD-1	PVPDDITVKQATEKCGD (SEQ ID NO:9)	hydrophobin	++	+++
HYD-2	ATYAGDVTDDIEGIL (SEQ ID NO:10)	hydrophobin	++	+
CAT-B-1	DEBDQLRFGFDLDP TKIVP (SEQ ID NO:15)	Catalase B	++	++
CAT-B-2	RIDNDLARRVARAIGV (SEQ ID NO:16)	Catalase B	++	++
ENO-1	KNVNETITGPALIKEND (SEQ ID NO:13)	Enolase	++	-
ENO-2	TSDFQIVGDDLTVTNPGR (SEQ ID NO:14)	Enolase	-	+
Peptide 2	KEGAEQSAPQAEHSTK (SEQ ID NO:8)	CssI	+++	+++
Peptide 1	KVAQEIIINPGPKVVT (SEQ ID NO:7)	CssI	++	++

*Reactivity of sera raised against the peptide against the surface of AfC or AfM

Table 4. Analysis of the ability of anti-IMDH B IgG to bind the surface of clinical isolates.

Strain Number	Original substratum	Pathogenicity (underlying disease):	Anti IMDH-B intensity	
			<u>Candida</u>	<u>Mycelium</u>
Isolate 46640	Human Lung	Aspergilloma	++	++
IHEM 1246	Outdoor air	-----	+	+
IHEM 2494	Human sputum	Allergic Bronchopulmonar Aspergillosis	++	++
IHEM 2739	Human sinus	Mycotic sinusitis	++++	++
IHEM 2895	Human bronchoaspiration (fungal ball)	Bronchitis	+++	+
IHEM 3007	Human lung	Pulmonary aspergillosis	-	+++
IHEM 4184	Human lung biopsy	Aspergillosis (heart transplant)	-	++
IHEM 4185	Human bone	Aspergillosis (heart transplant)	-	++
IHEM 4187	Human bronchial secretions	Aspergillosis (liver transplant)	+	+
IHEM 4699	Human bronchoaspiration	Aspergillosis (bone marrow transplant)	++	+
IHEM 4750	Human lung from autopsy	Aspergillosis (liver transplant)	+++	ND
IHEM 4756	Human sputum	Aspergillosis (marrow transplant)	-	+

Figure 1. The predicted protein sequences of CssI (A), hydrophobin (B), GAPDH-B (C), enolase (D), catalase B (E), catalase A(F), and isopropylmalate dehydrogenase B (G). X₁ is S or A and X₂ is L or I.

A

MLASFQFCILPRTYRTLLCSAGAGPLLIIQFVTVASALALAPTAVVARQGAAAFVTVNSIDVCPKKVAQEIIINPGPKVVTTTP
YTCDQVKLGHLGDLVSYNFDIEPLTKDTFPYCKALKVFDNEGCLGFPTLWIPLESPLDKCIPEHYFSDEVKX₁SIFQLDCRE
DAPVKKEPYGPKEGAEQSAPQAEHSTKQDAQQGSHQGEVQNSPKQEARQGSRAEAPKQEQEAEQASEAAPEKKASNPAD
SLGLGELTKVLGFR

B

VRFPVPDDITVKQATEKCGDQAQLSCCNKATYAGDVTIDIEGILAGTLKNLIGGGSGTEGLGLFNQCSKLDLQSPIIGIPIQ
DLVNQKCKQNIACCQNSPSDAVRFP

C

MATPKVGINGFGRIGRIVGLNSLSHGVDVAVNDPFIHVHYAAYMLKYDTTHGQFKGTIETYDQGLIVNGKKIRFYAEKD
PSQIPWSETGAAYIVESTGVFTTKEKASAHKGGAKKVIISAPSADAPMFVMGVNNTTYTSDIQVLSNASCTTNCLAPLA
KVINDKFGIVEGLMTTVHSYTATQKVVDAPSNKDWRGRTAAQNIISSSTGAAKAVGKVIPSLNGKLTGMAMRVPTSNVS
VVDLTCLRLEKASYDEIKQAIIKAASEEGELKNILGYTEDDVVSSDLNGDERSSIFDAKAGISLNPNFVKLVAWYDNEW

D

MPISKIHARSVYDSRGNPTVEVDVATETGLHRAIVPSGASTGQHEAHELKRDGDKTQWGGKGVKAVKNVNETIGPALIKENI
DVKDQSKVDEFLNKLDTANKSNLGNAILGVSLAVAKAGAAEKGVPLYAHISDLAGTKKPYVLPVFPQNLNGGSHAGGRL
AFQEFMIVPDSAPSFSEALRQGAEVYQKLKALAKKYGQSAGNVGDEGGVAPDIQTAEALDLITEAIEQAGYTGK
IKIAMDVASSEFYKADVKKYDLDFKNPESDPSKWLTYEQLADLYKSLAAKYPIVSIEDPFAEDDWEAWSYFYKTSDFQIVGD
DLTVTNPGRIKKAIELKSCNALLKVNQIGTLTESIQAAKDSYADNWGMVSHRSGETEDVTIADIAGVLRSGQIKTGAPCR
SERLAKLNQILRIEELGENTVYAGSKFRNAVNL

E

MRLTFIPSLIGVANAVCPYMTGELNRRDEISDGDAAAATEEFLSQYYLNDNDAMFTSDVGGPIEDQNSLSAGERGPTLLEDF
IFRQKIQRFDHERVPERAVHARGAGAHGVFTSYGDFSNITAASFLAKEGKQTPVFVRFSTVAGSRGSSDLARDVHGFPATRFY
TDEGNFDIVGNIPVFFIQDAILFPDLIHAVKPRGDNEIPQAATAHDSAWDFFSQQPSTMTLLWAMSGHIGIPRSF
RHVDGFGVHTFRFVTTDDGASKLVKFHWKSLQGKASMWEEAQQTSGKNPDMRQDLHDAIEAGRYPEWELGVQIMDEEDQLR
FGFDLLDPTKIVPEEFVPIITKLGMQLNRNPNRYFAETEQVMFQPGHIVRGVDFTEDPLLQGRFVSYLDLTQLNRHGGPNFEQ
LPINQPRVPVHNNNRDAGQMFIPLNPHAYS PKTSVNGSPKQANQTVGDGFFTA PGRTTSGKLVRVAVSSSFEDVWS
QPRFLFYNLSLPAEKQFVIDAIRFENANVKSPPVVKNNVILQLNRIDNDLARRVARAIGVAEPEPDTFYHNNKTADVGTFTGK
LKKLDGLKGVVLGSLVQHPGSVEGASTLRDLKDDGDVVLVAERLADGVDQTYSTSDAIQFDAVVVAAGAESLFAASSFTGG
SANSASGASSLYPTGRPLQILIDGFRFGKTVGALGSGTAALRNAGIATSRDGVYVAQSVTDDFANDLKEGLRTFKF
LDRFPVDH

F

MATKIAGGLHRAQEVLTQNTSSKSKKLVDLERDTADAHTQQPLTDDHGVRVSNTDQWLRVTNDRRTGPSLLEDQIAREKIHFR
DHERIPERVHARGTGAFGNFKLKESIEDLTYAGVLTDTSRNTPVFVRFSTVQSGRSADTVRDVRGFAVKFYTDEGNWDIV
GNIPVFFIQDAVKFPDFVHAVKPEPHNEVPQAQTAHNNFDFVYLHPEATHMFMWAMSDRAIPRSYRMMQGGFVN
TFALVNKEGKRHFVKFHWIPLHGVHSLVWDEALKLGGQDPDFHRKDLMEADNKAYPKWDFAIQVIPEEKQDDFEFDILDAT
KIWPENLVPLRVIGELELNRNVDEFFPQTEQVAFCTSHIVPGIDFTDDPLLQGRNFSYFDTQISRLGINWEELPINRPVCPV
LNHNRDGMHRITQGTVNYPNRFEAVPPTGKSGSGVGGGFTTYPQRVGEGIKNRALNDKFRHHNQALFYNSMS
EHEKLHMKKAFSFDLHCDPTVYERLAGHRLAETDLELAQKVAEMVGAPIPAKALKQNHGRRAPHLSTQTEFIKPNPTIASR
RIAIIGDGYDPVASTGLKTAIKAASALPFIIGTKRSAIYATEDKTSKGIIPDHHYDQGRSTMFDAFIPGGPHVATLRQN
GQIKYWISETFGHLKALGATGEAVDLVKETLSGTLHVQVASSQSPEPVEWYGVVTTAGGKQKPESFKESVQILKGAT
DFVGKFFYQISQHRNYQRELDGLASTIAF

G

MVTYINILVLPDGGIGPEVMTAEAVKVLKVFENEHRKFNLRQELIGGCSIDAHGKSVTEEVKKAALLESDAVLFAAVGGPKW
DHIRRGDLGPEGGLLQLRKAMDIYANLRPCSASSPSASIAKEFSPPRQEVIEGVDFVVVRENCGGAYFGKKIEEDYAMD
EWGYSEREIQRITRLX₁AEX₂ALRHNPWPVVISLIDKANVLASSRLWRRVVEKTMTEYQVQLVHQLADSASLILATNPRLN
GVILADNTFGDMISDQAGSIVGTGLVLPASLDGLPSETRKRTNGLYEPHGSAPTIAQNIANPVMILCVALMFRYSLDM
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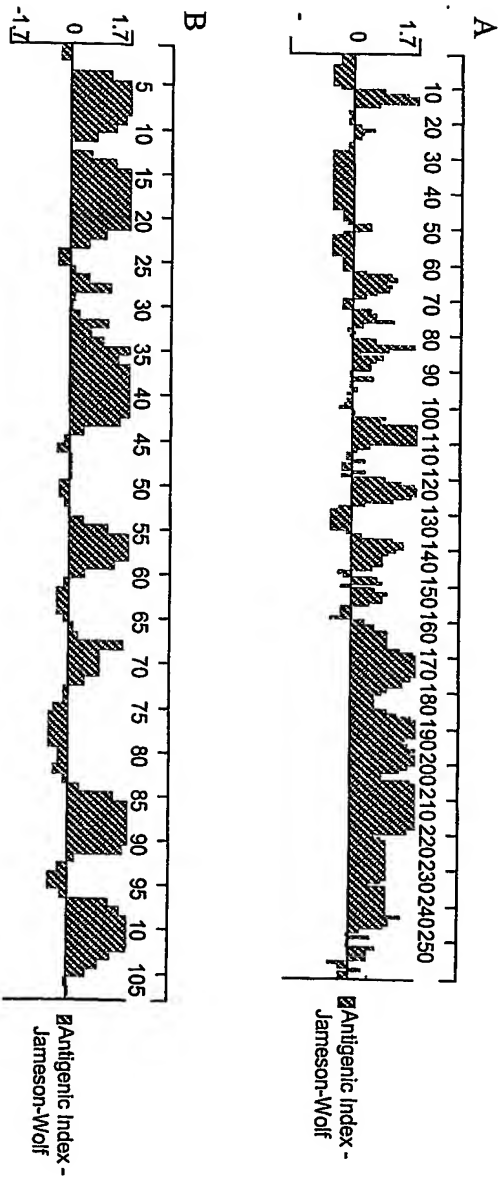


Figure 2. The predicted antigenicity indices of Csl (A) and hydrophobin (B) residues.

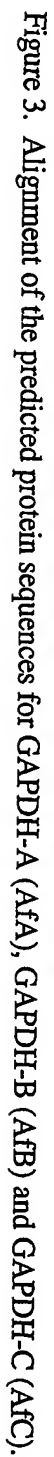


Fig. 4

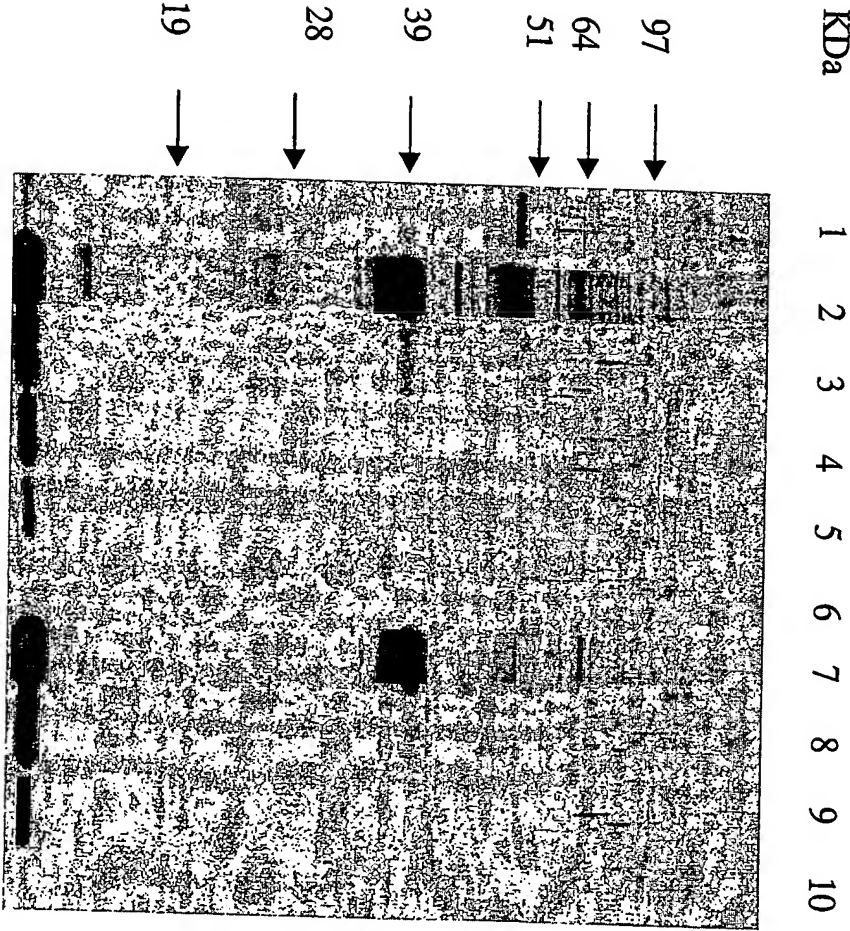


Fig. 5

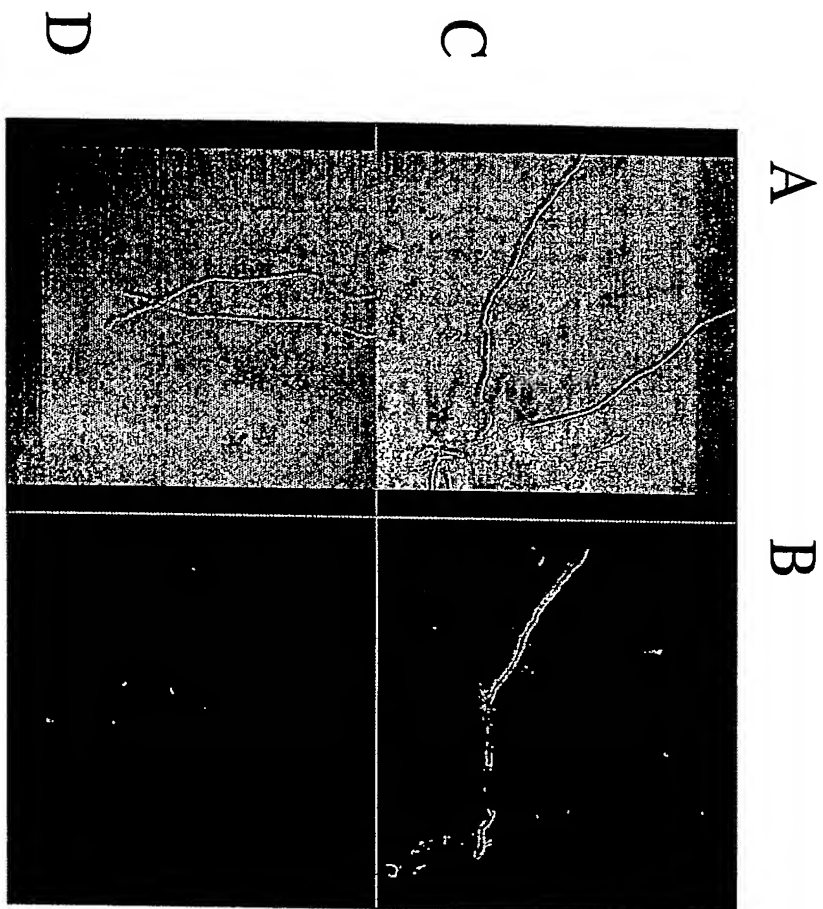
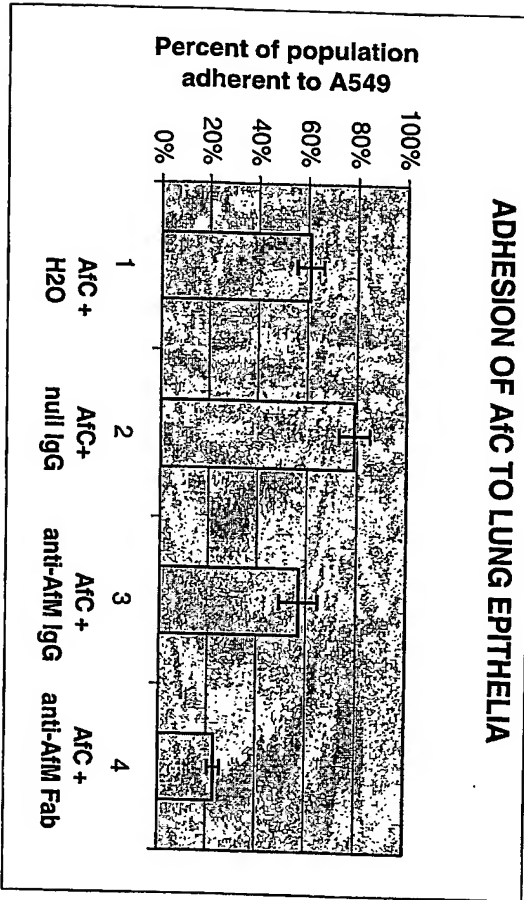
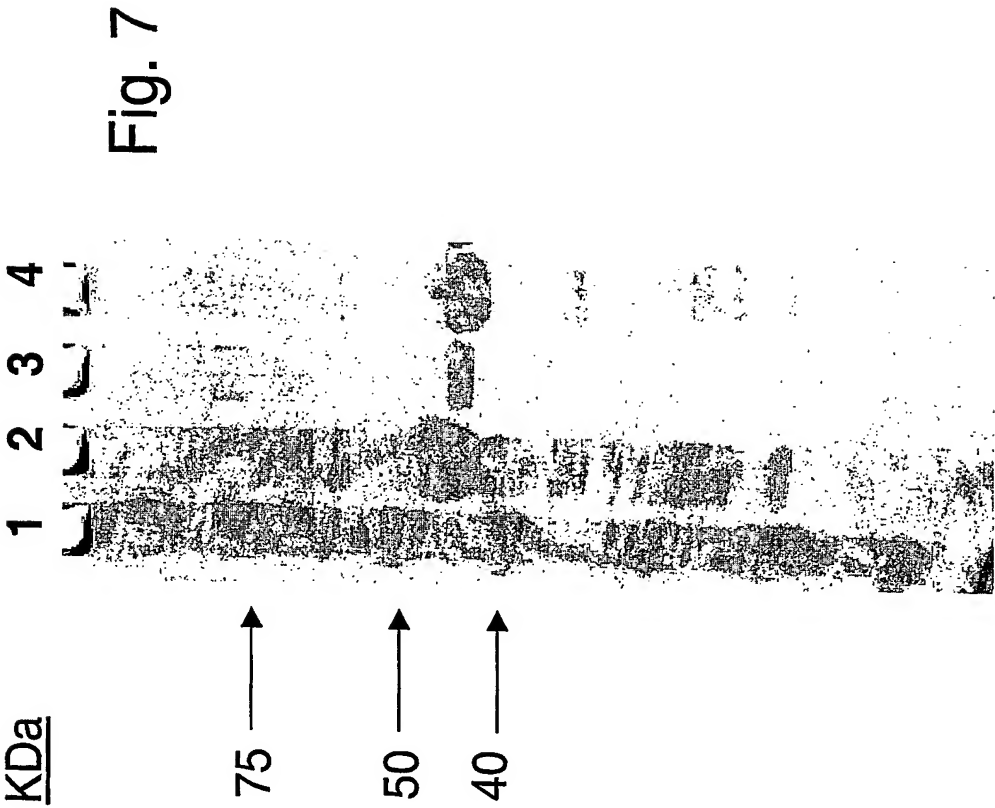


Figure 6





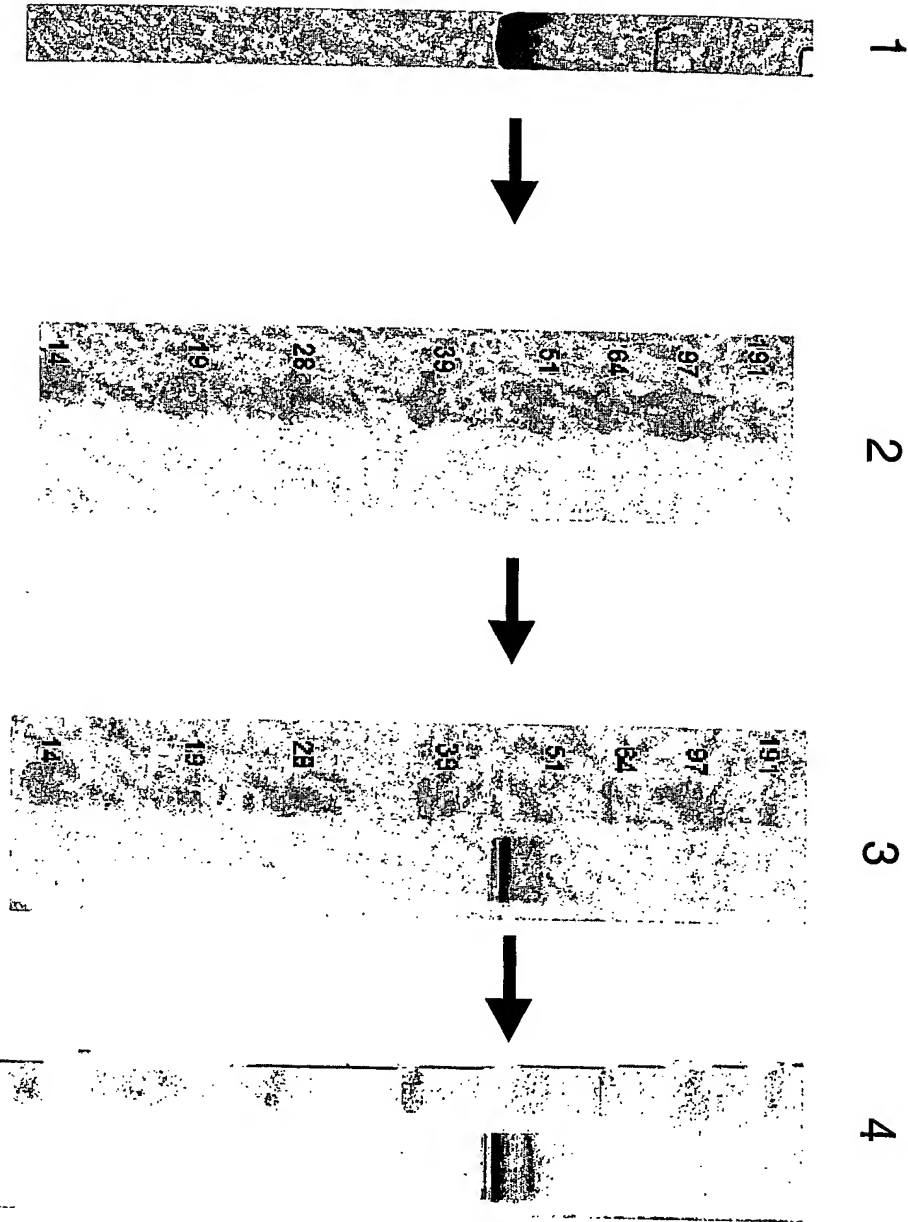
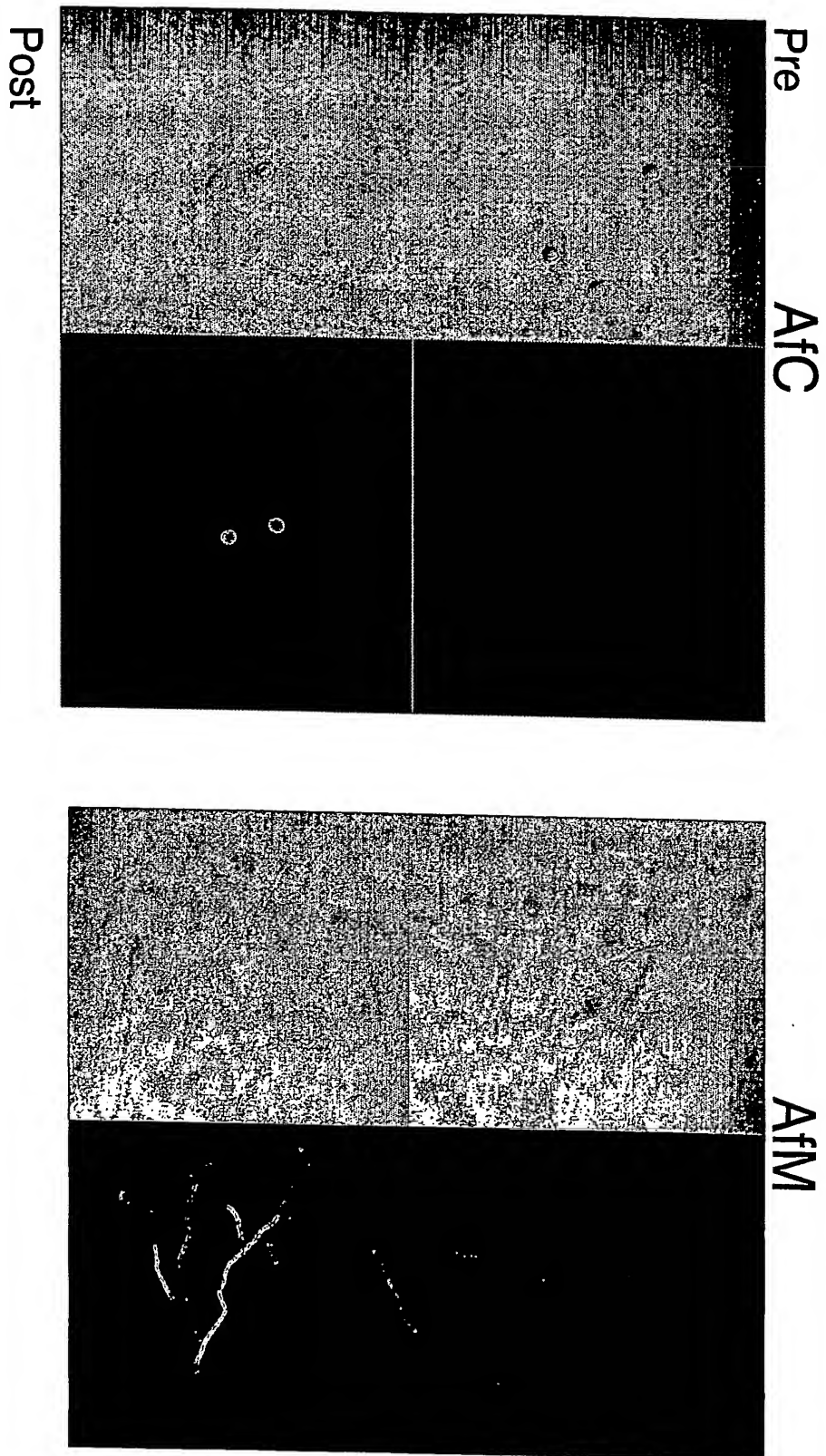


Fig. 8



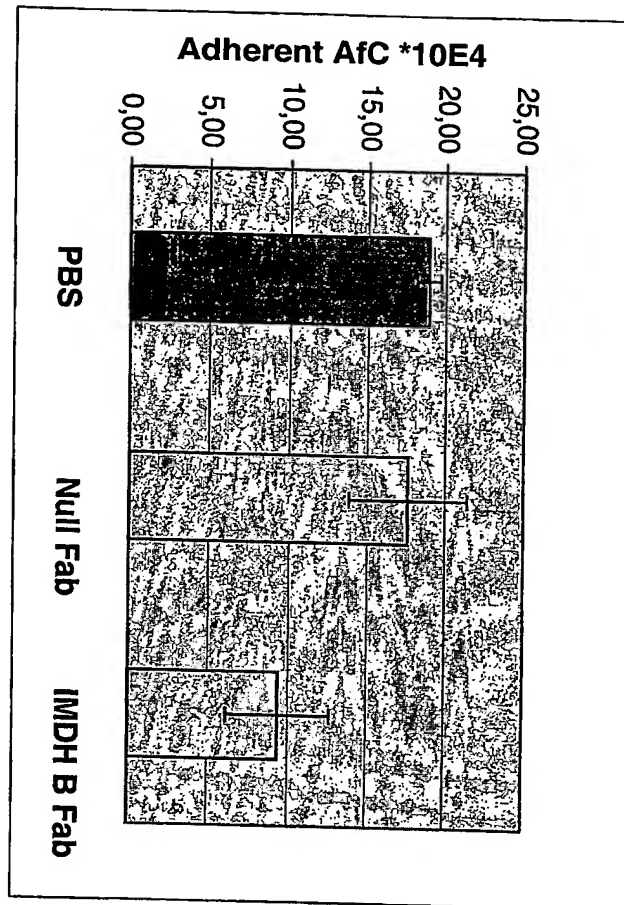


Fig. 10

Fig. 11

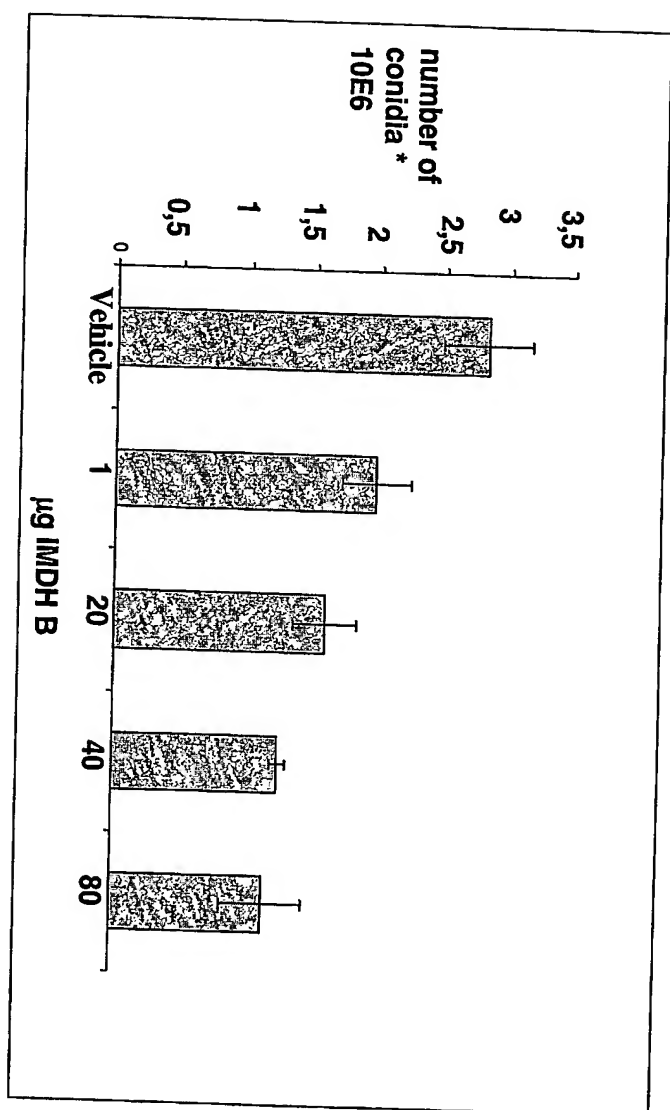


Figure 12

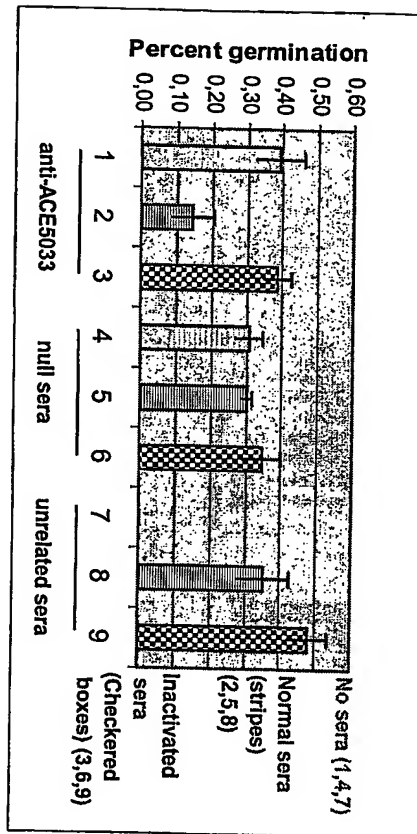


Figure 13

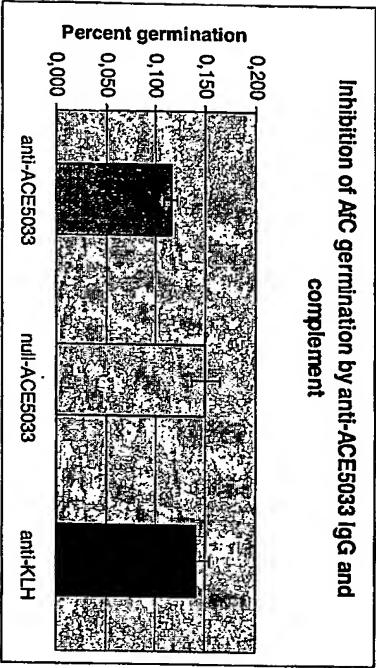


Fig. 14

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IMDHB1: 3 SYNIVVFAGDHC GPEVSS----VLRVIEKCRDDATFNLQDQLLGGVSSIDATGSPLTDEA 58
      +YNI+V GD GPEV + VL+V E + FNL+ +L+GG S IDA G +T+E
IMDHB2: 4 TYNILVLP GDGIGPEVMTEAVKVLKVFEN--EHRKFNL RQELIGGCS-IDAHGKSVTEEV 60

IMDHB1: 59 LNAAKNADAVLLGAIGGPKWG---TGAVRPEQGLLRRLRKEMGTFGNLRPCNFAAPSLV-- 113
      AA +DAVL A+GGPKW G PE GLL+LRK M + NLRPC+ ++PS
IMDHB2: 61 KKAALSDAVLFAAVGGPKWDHIRRGLDGPEGGLQLRKAMDIYANLRPCSASSPSASIA 120

IMDHB1: 114 -DGSPLRPEVCRGVDFNIIRELTGGIYFGDRKEDDGS GFAMDTPEPYSRAEIERITRLAAH 172
      + SP R EV GVDF ++RE GG YFG + E++ +AMD YS EI+RITRL+A
IMDHB2: 121 KEFSPFRQEVIEGVDFV VVRENC GGAYFGKKIEED--YAMDEWGYSEREIQRITRLSAE 178

IMDHB1: 173 LALQHNPPPLPVWSLDKANVLATSRLWRKT VTEVMAKEFPQLKVEHQLIDSAAMIMVKEPR 232
      +AL+HNPP PV SLDKANVLA+SRLWR+ V + M E+PQ+K+ HQL DSA++I+ PR
IMDHB2: 179 IALRHNPFPVVISL DKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLILATNPR 238

IMDHB1: 233 KLNGIVVTSNLF GDIISDEASVIPGSLGLLPSASLSGIP-DGKTKVNGIYEPHGSAPDI 291
      LNG+++ N FGD+ISD+A I G+LG+LPSASL G+P + + + NG+YEP HGSAP I
IMDHB2: 239 ALNGVILADNTFGDMISDQAGSIVGTLGVLP SASLDGLPSETRKRTNGLYEP THGSAPT I 298

IMDHB1: 292 AGKGIVNPVAAILSVAMMMQYSLNRMDDARA IETAVRN VIEAGIRTADIGGKSTTSEVGD 351
      AG+ I NPVA IL VA+M +YSL+ +A+ IE AV+ V++AGIRT D+GGKS T+EVGD
IMDHB2: 299 AGQNIANPVAMILCV ALMFRYSLDMETEAQRIEKAVQGVL DAGIRTPDLGGKSGTNEVGD 358

IMDHB1: 352 AVAAELE 358
      A+ A L+
IMDHB2: 359 AIVAALQ 365

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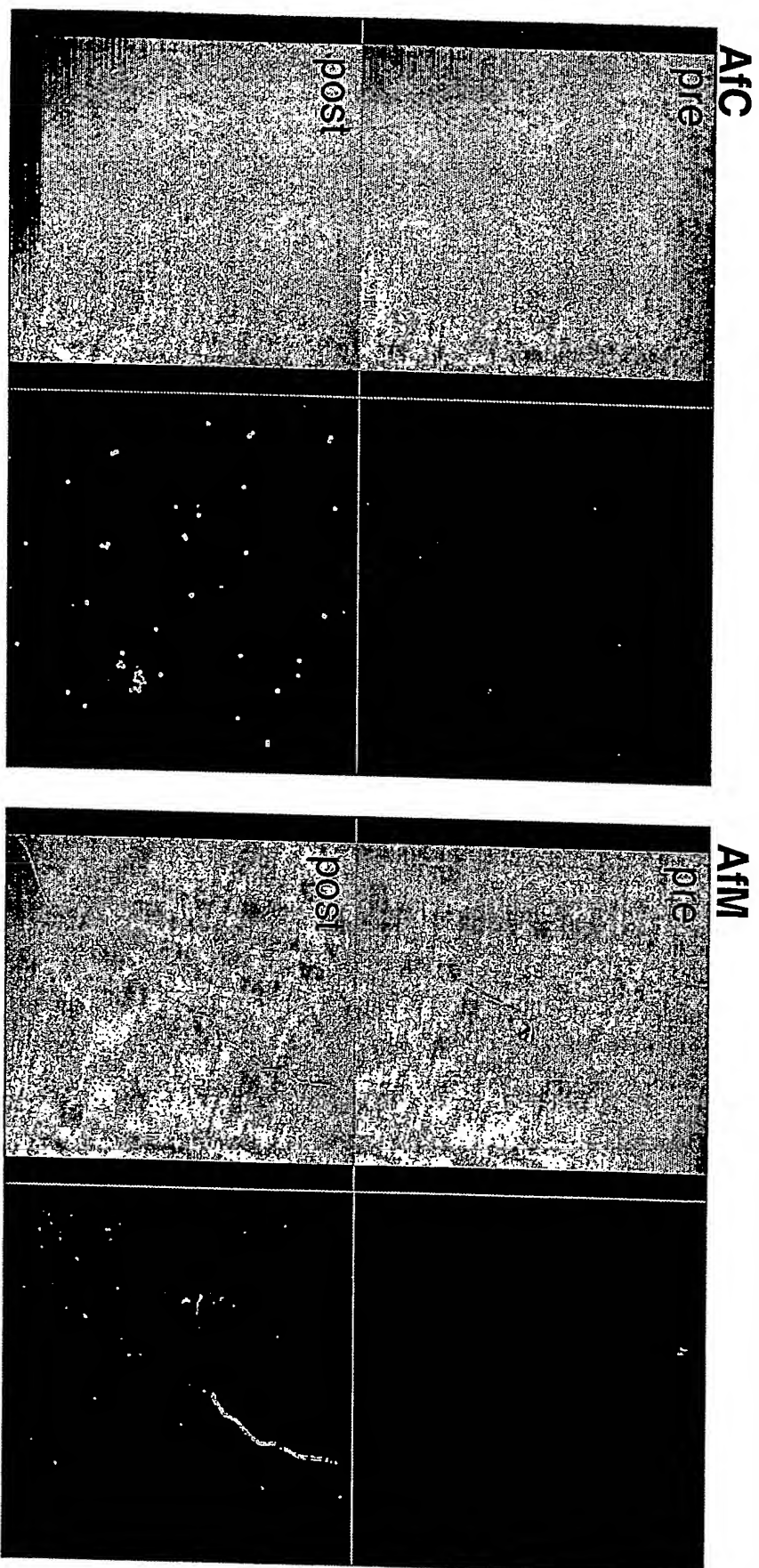
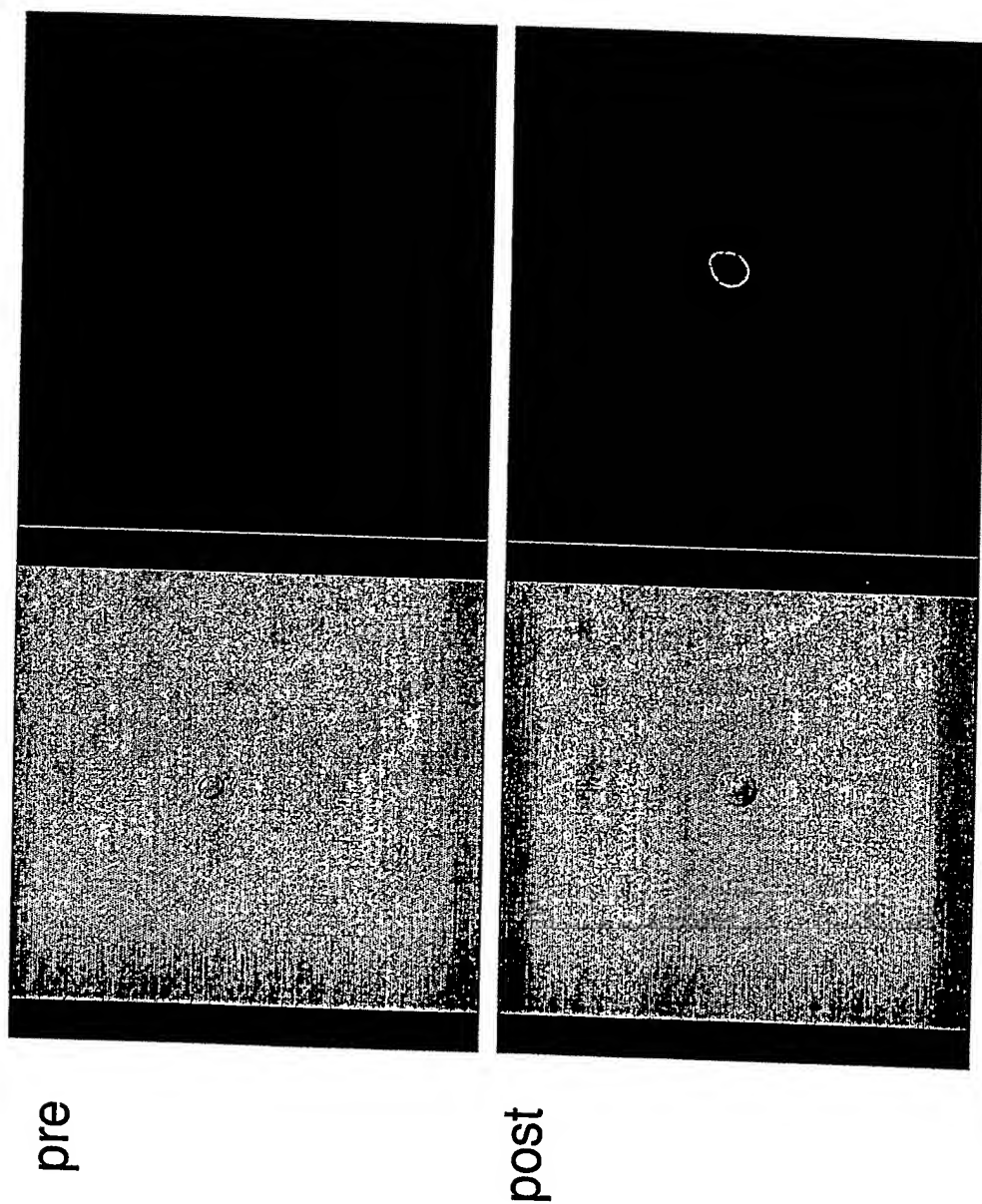


Fig. 15: Anti-GAP-B-2 (GAPDH)

Fig. 16
IHEM 3133



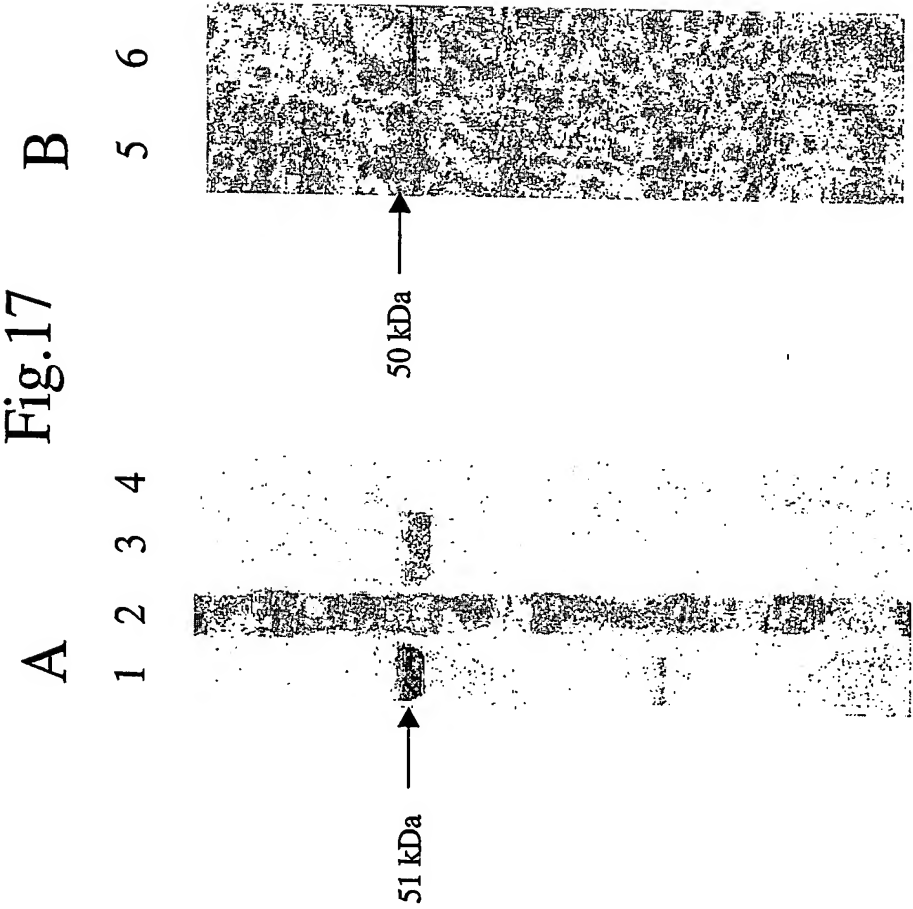


Figure 18**BLAST OF SEQ ID NO:36 AGAINST:**

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>orf19.7080 orf10262:179916-178795:e 1122 bp, 373 aa, contig 244073 bp
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Score = 335 bits (860), Expect = 1e-92

Identities = 185/368 (50%), Positives = 246/368 (66%), Gaps = 9/368 (2%)

Frame = +1

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V T I VLPD +G E++ EA+KVLK E + +F+ + LIGG +IDA G +
Sbjct: 7 VKTKTITVLPDGHVGTEIVNEAIKVLKAIEAATPYQKIQFDFKHHLIGGAIDATGVPLP 186

Query: 58 EEVKKAALSDAVLFAAVGGPKWDHIRRGLDGPEGGLLQLRKAMDIYANLRPCSASSPSA 117
++ ++A SDAVL AVGGPKW G PE GLL++RK +++YAN+RPC+ +S S
Sbjct: 187 DDALESAKSSDAVLLGAVGGPKWG---TGTVRPEQGLLKIRKELNLYANIRPCNFASDSL 357

Query: 118 SIAKEFSPFRQEVIEGVDFVVRVRENCGGAYFGKKIEEDY-----AMDEWGYSEREIQRI 172
E SP + EV++G + ++VRE GG YFG++ E+E+ A D Y+ E+ RI
Sbjct: 358 L---ELSPLKAEVVKGTNLIIVRELVGGIYFGERQEQEESDKKTAWDTEKYTVDEVTRI 528

Query: 173 TRLSAEIALRHNPPWPVISLIDKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLI 232
TR++A +AL+HNPP P+ SLIDKANVLASSRLWR+ V+K ++ E+P + + HQL DSA++I
Sbjct: 529 TRMAAFMALQHNPPPLPIWSLIDKANVLASSRLWRKTVDKVISEEFPALSVQHQLIDSAAMI 708

Query: 233 LATNPRALNGVILADNTFGDMISDQAGSIVGTLGVLPSASLDGLPSETRKRTNGLYEPH 292
L NP LNG+I+ N FGD+ISD+A I G+LG+LPSASL LP GLYEP H
Sbjct: 709 LIQNPTKLNIGIITSNMFGDIISDEASVIPGSLGLLPSASLASLPD--TNTAFGLYEPCH 882

Query: 293 GSAPTIAGQNIANPVAMILCVALMFRYSIDMETEAQRIEKAVQGVLDAGIRTPDLGGKSG 352
GSAP + N NP+A IL A M R SLD EA+ +E+AV+ VLD+GIRT DL G S
Sbjct: 883 GSAPDLPA-NKVNPIATILSAASMLRLSLDCVKEAEALEEAVKQVLDGIRTDLRGTSS 1059

Query: 353 TNEVGDAI 360
T EVGDAI
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Candida seq orf10262:179916-178795**1**

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GIYFGER
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DKVISEEFPALS
VQHQLIDSAAMILIQNP
TKLNGIITSNMFGDIISDEASVIPGSLGLLPSASLASLPD
TNTAFGLYEPCHGSAP
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Figure 19**BLAST OF SEQ ID NO:36 AGAINST:**

Elrond pep

A. nidulans

>AnrP4374925 LE3B_ASPNG 3-isopropylmalate dehydrogenase B (Beta-IPM
dehyd
Length = 370

Score = 597 bits (1540), Expect = e-171

Identities = 295/364 (81%), Positives = 326/364 (89%), Gaps = 1/364 (0%)

Query: 4 TYNILVLPDGGIGPEVMT EAVKVLKVFENEHRKFNLRQELIGGCSIDAHGKSVTEEVKKA 63
+YNILVLPDGGIGPEVMT EA K+L +F +F + ELIGGCSID HGKSVT+ V A
Sbjct: 5 SYNILVLPDGGIGPEVMAEATKILSLFNTSTVRFRTQTELIGGCSIDTHGKSVTQAVLDA 64

Query: 64 ALESDAVLFAAVGGPKWDHIRRGLDGP EGGLQLRKAMDIYANLRPCSASSPSASI AKEF 123
A+ SDAVLFAAVGGPKWDHIRRGLDGP EGGLQ+RKAMDIYANLRPCS SPS IA++F
Sbjct: 65 AVSSDAVLFAAVGGPKWDHIRRGLDGP EGGLQVRKAMDIYANLRPCSVDSPSREIARDF 124

Query: 124 SPFRQEVIEGVDFV VVRENC GGAYFGKKIEEDYAMDEWGYSEREIQRITRLSAEIALRH 183
SPFRQ+VIEGVDFV VVRENC GGAYFGKK+EE+DYAMDEWGYS EIQRITRLSAE+ALRH
Sbjct: 125 SPFRQDVIEGVDFV VVRENC GGAYFGKKVEEDYAMDEWGYSASEIQRITRLSAELALRH 184

Query: 184 NPPWPVISL DKANVLASSRLWRRVVEKTMTEY P QVKLVHQLADSASLILATNPRALNGV 243
+PPWPVISL DKANVLASSRLWRRVVEKTM+ EYPQVKLVHQLADSASLI+ATNPRALNGV
Sbjct: 185 DPPWPVISL DKANVLASSRLWRRVVEKTMSE EYPQVKLVHQLADSASLIMATNPRALNGV 244

Query: 244 ILADNTFGDMISDQAGSIVGTLGVLP SASLDGLPSE-TRKRTNGLYEP THGSAPTIAGQN 302
ILADNTFGDM+SDQAGS+VGTLGVLP SASLDGLP +++ +GLYEP THGSAPTIAG+N
Sbjct: 245 ILADNTFGDMVSDQAGSLVGTLGVLP SASLDGLPKPGEQRKVHGLYEP THGSAPTIAGKN 304

Query: 303 IANPVAMILCVALMFRYS LDMETEAQRIE KAVQGVLDAGIRTPDLGGKSGTNEVGDAIVA 362
IANP AMILCVALMFRYS +ME EA++IE AV+ VLD GIRT DLGG +GT E GDA+VA
Sbjct: 305 IANPTAMILCVALMFRYSFNMEAEARQIEAAVRTVLDKGIRTS DLGGSTGTREFGDAVVA 364

Query: 363 ALQG 366
AL+G
Sbjct: 365 ALKG 368

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ALRHDPPWPVISL DKANVLASSRLWRRVVEKTMSE EYPQVKLVHQLADSASLIMATNPRA
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AVVAALKGEL

Figure 20**BLAST OF SEQ ID NO:36 AGAINST:**

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 >AnRP3711474 hypothetical protein [Aspergillus oryzae]
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 +++YNI+V GD GPEV EA+KVL+ E N FNL+ L+GG SIDA G +T+E
 Sbjct: 1 MSSYNIVVFGGDHCGPEVTAEAIKVLRAVEKNRDVTFNLQDHLGGASIDATGSPLTDEA 60

Query: 61 KKAALSDAVLFAAVGGPKWDHIRGLDGPGLLQLRKAMDIYANLRPCSASSPSASIA 120
 AA +DAVL A+GGPKW G PE G+L+LRK M + NLRPC+ ++PS
 Sbjct: 61 LNAAKNADAVLLGAIGGPKWG---TGAVRPEQGILKLRKEMGTFGNLRPCNFAAPSLV-- 115

Query: 121 KEFSPFRQEVIEGVDFVVRRENCGGAYFGKKIEBED--YAMDEWGYSEREIQRITRLSAE 178
 E SP R +V GV+F ++RE GG YFG++ E++ YAMD YS EI+RI RL+A
 Sbjct: 116 -ESSPLRADVCRGVNFNIIRELTGGIYFGERKEDDGSYGAMDEPYSRAEIERIIRLAH 174

Query: 179 IALRHNPWPVISLSDKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLILATNPR 238
 +AL+H+PP PV SLDKANVLA+SRLWR+VV + M E+PQ+K+ HQL DSA++I+ NPR
 Sbjct: 175 LALQHDPPPLPVWSLDKANVLATSRLWRKVVTEVMAKEFPQLKIEHQLIDSAAMIMVKNPR 234

Query: 239 ALNGVILADNTFGDMISDQAGSIVGTLGVLPSASLDGLPSETRKRTNGLYEPHGSAPTI 298
 LNG+++ N FGD+ISD+A I G+LG+LPSASL G+P + + NG+YEP HGSAP I
 Sbjct: 235 QLNGIVVTSNLFVDIISDEASVIPGSLGLLPSASLSGIP-DGNSKVNGIYEPHGSAPDI 293

Query: 299 AGQNIANPVMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSGTNEVGD 358
 AG+ I NPVA IL VA+M +YS + EA+ IE+AV V+++G+RT D+GGK+ T EVGD
 Sbjct: 294 AGKGIVNPVAAILSVAMMMQYSFGLFAEARAIEQAVSNVIESGVRTGDIGGKATTAEVGD 353

Query: 359 AIVAALQ 365
 A+ A L+
 Sbjct: 354 AVAAELE 360

Oryzae seq >AnRP3711474

MSSYNIVVFGGDHCGPEVTAEAIKVLRAVEKNRDVTFNLQDHLGGASIDATGSPLTDEA
 LNAAKNADAVLLGAIGGPKWGTGAVRPEQGILKLRKEMGTFGNLRPCNFAAPSLVESSPL
 RADVCRGVNFNIIRELTGGIYFGERKEDDGSYGAMDEPYSRAEIERIIRLAHLALQHD
 PPLPVWSLDKANVLATSRLWRKVVTEVMAKEFPQLKIEHQLIDSAAMIMVKNPRQLNGIV
 VTSNLFVDIISDEASVIPGSLGLLPSASLSGIPDGNSKVNGIYEPHGSAPDIAGKGIVN
 PVAAILSVAMMMQYSFGLFAEARAIEQAVSNVIESGVRTGDIGGKATTAEVGDAAVAELE
 KLLK

Figure 21**BLAST OF SEQ ID NO:36 AGAINST:**

□ BLASTP:temp_job2_pep_9_AnRP4379986
>AnRP4379986 conserved hypothetical protein [Aspergillus nidulans
FGSC A4
Length = 357

Score = 149 bits (376), Expect = 1e-36
Identities = 113/369 (30%), Positives = 186/369 (49%), Gaps = 27/369 (7%)

Query: 1 MVTYINILVLPDGGIGPEVMTEAVKVLKVFENEHRKFNLRQELIGGCS--IDAHGKSVTE 58
M TY I +P DGIGPEV+ V VLK ++ + F+L + S A GK + +
Sbjct: 1 MAKTYRIATIPADGIGPEVIDAGVIVLKALADKLQSFSLDFTHLDSWSETFKATGKYIPD 60

Query: 59 EVKKAALSDAVLFAAVGGPKW-DHIRRLDGPPEGGLQLRKAMDIYANLRPCSASSPSA 117
+ ++DA+LF AVG P DHI G L + + YAN+R P+
Sbjct: 61 GGLEVLKKNDAILFGAVGAPDVPDHISLW-----GLRLAICQPFQYANVR-----PTR 109

Query: 118 SIAKEFSPFRQEVIEGVDFVVRVRENCGGAYFGK-----KIEEEDYAMDEWGYSEREIQRI 172
+ SP R+ +D+V+VREN G Y G+ + + A + +S + ++RI
Sbjct: 110 VLRGTQSPLRKCNTGDLDWVIVRENSEGEYAGQGGRSHRGHPWEVATEVAIFSRQGVVERI 169

Query: 173 TRLSAEIALRHNPPWPVISLIDKANVLASSRLWRRVVEKTMTEYPOVKLVHQLADSASLI 232
R + E A + P + + K+N + + V + ++P+V + L D+ +
Sbjct: 170 MRFAFETAAR-RPRKLLTVVTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTTR 228

Query: 233 LATNPRALNGVILADNTFGDMISDQAGSIVGTGLVLPASLDGLPSETRKRTNGLYEPH 292
+ P +L+ I+A N D++SD A ++ G++G+ P+++LD ++ ++EP H
Sbjct: 229 MVLKPESLD-TIVASNLHADILSDLAALAGSIGIAPTSNLD-----PTRQNPSMFEPH 282

Query: 293 GSAPTIAQONIANPVAMILCVAMLFYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSG 352
GSA I G+ IANPVA A M + L + A ++ + V+ V ++GI T DLGG +
Sbjct: 283 GSAFDITGKGIANPVATFWTAAEMLEW-LGEKDAADKLMQCVESVCEGILTADLGGTAT 341

Query: 353 TNEVGDAIV 361
T EV A+V
Sbjct: 342 TKEVTSADV 350

Nidulans seq >AnRP4379986

MAKTYRIATIPADGIGPEVIDAGVIVLKALADKLQSFSLDFTHLDSWSETFKATGKYIPD
GGLEVLKKNDAILFGAVGAPDVPDHISLWGLRLAICQPFQYANVRPTRVLRGTQSPLRK
CNTGDLDWVIVRENSEGEYAGQGGRSHRGHPWEVATEVAIFSRQGVVERIMRFAFETAAR
PRKLLTVVTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTTRMVLKPESLDTIV
ASNHLHADILSDLAALAGSIGIAPTSNLDPTRQNPSMFEPHGSAGFDITGKGIANPVATF
WTAAEMLEWLGEKDAADKLMQCVESVCEGILTADLGGTATTKEVTSADVVEINRLN

Figure 22**BLAST OF SEQ ID NO:36 AGAINST:**

>gnl|TIGR_222929|contig:1772:c_posadasii *Coccidioides posadasii* C735
 unfinished fragment of genome
 Length = 119053

Score = 286 bits (732), Expect(2) = e-128

Identities = 146/233 (62%), Positives = 173/233 (74%), Gaps = 24/233 (10%)

Frame = -3

Query: 160 AMDEWGYSTTEIQXXXXXXXXXXXXHDPWPVISLTKANVLASSRLWRRVVENTISVEYP 219
 AMDEWGYST E+Q HDPPWPVIS+DKANVLASSRLWRRVVE T++ E+P
 Sbjct: 33806 AMDEWGYSTQEVQRIARLAHVALRHDPWPVISMDKANVLASSRLWRRVVEKTLTTEFP
 33627

Query: 220 QVKLVHQLADSASLIMATDPRVLNGVILADNTFGDMLSDQAGSLIGTLGVLPASLDGLP 279
 QVK HQLADSASLIMAT+PR LNGV+LADNTFGDMLSDQAGS++G+LGVLPASL G+P
 Sbjct: 33626 QVKFSHQLADSASLIMATNPRSLNGVLLADNTFGDMLSDQAGSIVGSLGVLPASLSGIP
 33447

Query: 280 HPGKQE--KVRGLYEPHGSAPT-----IAGKNIANPTAMILC 315
 +++ K LYEPHGSAPT IAGKN+ANP AMILC
 Sbjct: 33446 GEKRKDGKKSALYEPHGSAPT*VNCDLWMINTARKANRLD*CRIAGKNVANPLAMILC
 33267

Query: 316 VSLMFRYSFNMENEARQIEDAVRAVLDRGLRTPDLGGNSSTQEFDAVVAALQ 368
 V++MFRYSFNME EA+ IE+AV A L+ G+RTPDLGG + T + G+A+VA ++
 Sbjct: 33266 VAMMFRYSFNMEEPAKAIENAVTATLEAGIRTPDLGGKAGTTDVGNAIVAHIK 33108

Query: 4 TRAYNILVLPDGGIGPEVMAEAIKVLRTFNSSSMQFHLQEELIGGISIDTHGHSVTQFXX 63
 ++ YNIL LPDGGIGPE+MAEAIKVL+ F+S ++ F+L+ ELIGG SID HG +T
 Sbjct: 34383 SKTYNILTLPDGGIGPEIMAEAIKVLQAFSSPNLNFNLRLNELIGGCSIDAHGTPITDAVK
 34204

Query: 64 XXXXXXXXXXXXXXXGGSKVDHIRRGLDGPGEGLLQVRKAMDIYANLRPCSVDVPSREIAR 123
 GG K D RRGL+GPEGGLLQ+RK +D+Y N+RPCS DV ++R
 Sbjct: 34203 QAALESDAVLFAVGGPKWDSSRRGLEGPEGGLLQLRKVLDVYGNVPCSTDV-CASVSR
 34027

Query: 124 DFSPFRQEVIEGVDFVVVVRENCGGAYFGKKVEEENY 159
 +FSP+R EV+EGVDFVV+RENCGGAYFGK VE+E+Y
 Sbjct: 34026 EFSPYRTEVVEGVDFVVLRENCGGAYFGKXVEDEDY 33919

Coccidioides

2

SKTYNILTLPDGGIGPEIMAEAIKVLQAFSSPNLNFNLRLNELIGGCSIDAHGTPITDAVKQAALESDAVL
 FASVGGPKWDSSRRGLEGPEGGLLQLRKVLDVYGNVPCSTDVCASVSREFSPYRTEVVEGVDFV
 VLRENCGGAYFGKXVEDEDYAMDEWGYSTQEVQRIARLAHVALRHDPWPVISMDKANVLASSR
 LWRRVVEKTLTTEFPQVKFSHQLADSASLIMATNPRSLNGVLLADNTFGDMLSDQAGSIVGSLGVLP
 SASLSGIPGEKRKDGKKSALYEPHGSAPT*VNCDLWMINTARKANRLD*CRIAGKNVANPLAMILC
 VAMMFRYSFNMEEPAKAIENAVTATLEAGIRTPDLGGKAGTTDVGNAIVAHIK

Figure 23 SEQ ID NO:36 against: Cryptococcus >chr01b.b3501.031220.C11
(289426 bp) Length = 289426

Score = 183 bits (465), Expect(3) = 3e-68 Frame = +3
Identities = 113/258 (43%), Positives = 144/258 (55%), Gaps = 39/258 (15%)

Query: 148 FGKKIE--EEDYAMDEWGYSEREIQRITRLSAETALRHNPFPWFVISLTKANVLASSRLWR 205
FG++ E +E A D+ YS+ EI+RITR++A+IAL PP P+ S+DKANVLA+SRLWR
Sbjct: 173334 FGERQETNDEGVAWDQCIYSKPEIERITRVAAQIALAAEPPLPITSVDKANVLATSRLWR 173513

Query: 206 RVVEKTMTEYPQVKLVHQLADSASLILATNPRLNGVILADNTFGDM----- 253
+ V + M EYPQ+KL HQL DSA++I+ NPR LNGV+L +N FGDM
Sbjct: 173514 KTVSELMAKEYPQLKLEHQLVDSAAMIMIANPRKLNGLVLLTENMFGDM*VLSMVTKYRC* 173693

Query: 254 -----ISDQAGSIVGTGLVLPASLDGLPSETRKRTNGLYE-----PTHGS 294
S A + L + P LP ++ HGS
Sbjct: 173694 VCVVFLTKAPSSPAPLVSSLLRLSPVPPTLSLPPVWMSRSTIFPFLTYPN*PLCSIHGS 173873

Query: 295 APTIAGQNIANPVMILCVALMFRYSLDMETEAQRIEKAVQGVLDAG-----IRTPDLG 348
AP IAGQ IANP+ IL A+M RYSL EA IE+AVQ VLD+ RT DLG
Sbjct: 173874 APDIAGQGIANPIGTILSAAMMLRYSLGKGREALIEQAVQKVLDSEAESGGFDYRTKDLG 174053

Query: 349 GKSGTNEVGDAIVAALQG 366
G+ T EVGD +V L+G
Sbjct: 174054 GQRSTKEVGDKVVEVLKG 174107

Query: 15 IGPEVMTEAVKVLKFENEHR-KFNLRQELIGGCSIDAHGKSVTEEVKKALESDAVLFA 73
IGPEV+ EAV+VL+ N K +L+ GG +ID HG + +E KA E+DAVL
Sbjct: 172844 IGPEVVAEAVRVLETIVNHSIDLKLDLKSDFGGAAIDNHGVPLPDETLKACKEADAVLMG 173023

Query: 74 A-----VGGPKWDHIRGLDGPEGGLQLRKAMDIYANLRPCSASSPS 116
A VGGPKW G PE G+L+LRK + +YAN+RP A+ S
Sbjct: 173024 ACDFLAIRIKS*TA*KGSVGGPKWGV---GPNRPEQGILKLRKELGLYANIRP--ANFAS 173188

Query: 117 ASIAKEFSPFRQEVIEGVDFVVRNCGG 145
S+ K SP +++ G D +V+RE GG
Sbjct: 173189 ESLLKR-SPLKEDTARGTDIIVLRELIGG 173272

Query: 244 ILADNTFGDMISDQAGSIVGTGLVLPASLD-----GLPS---ETRKRTNGLYEPH 292
+L + +GD++SD + ++G LG+ PS ++ G PS K ++E H
Sbjct: 238292 LLIPHRYGDILSDLSAGLIGGLGLTPSGNIGKVSLSHDYGSPSIELTGDK*DASIFEAVH 238471

Query: 293 GSAPTIAQNIANPVMILCVALMFR----- 318
GSAP I G+ +ANP A++L +M R
Sbjct: 238472 GSAPDIEGKGLANPTALLSSLMMLR*VTQIPSVIVPALYPSVPDHTHPLARNVADLFVH 238651

Query: 319 YSLDMETEAQRIEKA---VQG-----VLDAGIRTPDLGGKSGTNEVG 358
+ + A +IEKA V G + + T DLGK+GT E D
Sbjct: 238652 RHMSLYELADKIEKAALSVSGETPWLFTFEMLIQVS*TIAEGKAITRD LGGKAGTKEYTD 238831

Query: 359 AIVAAL 364
AI++ L
Sbjct: 238832 AILSKL 238849

Query: 95 LQLRKAMDIYANLRPCSASSPSASIAKEFSPFRQEVIEGVDFVVRNCGGAYFGKKIEE 154
L LR+ ++AN+RPC SI +P+ + V+ V++REN G Y G IE
Sbjct: 237609 LTLRRTFSLFANVRPC-----VSIKGYKTPY-----DNVNTVLIRENTEGEYSG---IEH 237749

Query: 155 E 155
E
Sbjct: 237750 E 237752

Query: 5 YNILVLPDGGIGPEVMTEAVKVLK 28
Y + ++PGDGIGPE+ ++ K
Sbjct: 237256 YTVTLIPDGGIGPEIANSVKQIFK 237327

Query: 4 TYNILVLPDGGIG 16
++ I VLPDGGIG
Sbjct: 172752 SFKITVLPDGGIG 172790

Clustalw of sequences of figure 18-22

[illegible]

Figure 25 Continuation from figure 24

```
temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

LDKANVLASSRLWRRVVEKTMSEEPQVKLVHQLADSLIMATNPRALN
LDKANVLATSLWRKVVTEVMAKEFPQLKIEHQLIDSAAMIMVKNPRQLN
VTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTTRMVLKPESLD
LDKANVLASSRLWRKTVDKVISEEPPALSVQHQLIDSAAMILIQNPTKLN
MDKANVLASSRLWRRVVEKTLTTEFPQVKFESHQLADSLIMATNPRSLN
: ** * .. : * : : : * : : * : : * : : * : : * :
GVLLADNTFGDMVSDQAGSLVGTGLVLPASLDGLP--KPGEQRKVHGGLY
GIVVTSNLFGDIIISDEASVIPGSLGLLPASLSGIP----DGNSKVNGIY
-TIVASNLHADILSDLAALAGSIGIAPTNSLDPTR-----QNPSMF
GIITSNMFGDIIISDEASVIPGSLGLLPASLASLP----DTN-TAFGLY
GVLLADNTFGDMLSDQAGSIVGSLGVLPSASLSGIPGEKRDGKKSYALY
: : : * .. : * : : * : : * : : * : : * : :
EPTHGSAPTIIAGKNITANPTAMILCVALMFRYSFNMEAEARQIEAAVRTVL
EPIHGSAFDIAGKGIWNPVAAILSVAMMQYSFGLFAEARAIEQAVSNVI
EPIHGSAFDITGKGIANPVATFWTAAEMLEWLG-EKDAADKLMQCIVESVC
EPCHGSAPDLPAN-KVNPIATILSAA SMLRLSLDCVKEAEAEAVKQVL
EPTHGSAPT-----
** ****

DKGIRTSDLGGSTGTREFGDVAVVAAKKG
ESGVRTGDTGGKATTAEVGDVAAAELE-
ESGILTADLGGTATTKEVTSVV-----
DSGIRTADLRGTSSTTEVGDAI-----
```